

# Practical benefits of a genome sequence for the white potato cyst nematode *Globodera pallida*



A collaborative project between SCRI, Leeds University, Rothamsted Research and the Wellcome Trust Sanger Institute

Scottish Crop Research Institute

UNIVERSITY OF LEEDS

ROTHAMSTED RESEARCH

## Introduction

The white species of the potato cyst nematode - *Globodera pallida* - is an increasing problem to UK potato growers and is the most important nematode pathogen of UK agriculture. (Figure 1).

We believe that a new approach to management of *G. pallida* is required and that development of new control strategies requires a step change in the way we approach the problem.

A consortium of leading UK researchers has therefore been established that aims to obtain a genome sequence for *G. pallida*. This consortium consists of three of the major UK plant nematology centres (SCRI, Leeds University and Rothamsted Research) and the Wellcome Trust Sanger Institute, the only UK genome sequencing centre.

Here we outline the practical benefits that may emerge from a *G. pallida* sequencing project

Figure 1: Damage caused to potato plants by potato cyst nematodes (right)...



...and cysts of the nematode on potato roots (left).

## Examples of practical outputs - why sequence PCN?

### New control strategies

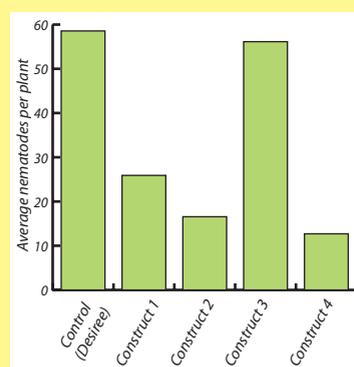
A genome sequence will provide researchers with details of all the genes present in PCN. As well as telling us a great deal about the underlying biology of the nematode this will provide us with a complete list of the potential nematode targets for novel control strategies.

Comparative genomics - comparing the genes of PCN with those in other (non-parasitic) nematodes - will help us identify those genes important for parasitising plants. This will help development of new, more specific control products. Comparing the genes used by nematodes and (for example) blight pathogens used to attack plants may also allow development of new generic control options.

Computer software used by the WTSI will allow identification of important nematode enzyme pathways that could be targets for new nematicides.

Partners in the project have a proven track record of developing new control options based on targeting well characterised nematode products (Figure 2).

Figure 2: Replication of *G. pallida* on control and transgenic plants containing constructs targeting a novel nematode gut protein. Figures are means of 5 replicates. Three of the four constructs tested provide statistically significant levels of control



### Natural Resistance

Natural resistance genes offer the most practically useful and environmentally benign means of controlling PCN (and other pathogens). Unfortunately, effective natural resistance against *G. pallida* has been extremely difficult to find and transfer to commercially viable cultivars.

Resistance genes operate by detecting specific nematode (or other pathogen) products ("avirulence genes").

Once these avirulence genes are detected, defence pathways are initiated leading to death of the tissues on which the nematode needs to feed (the nematode feeding site - see Figure 3).

A *G. pallida* genome sequence will provide a complete list of the potential nematode avirulence genes that trigger resistance in plants.

Identification of avirulence genes will allow functional screens for germplasm carrying resistance genes making plant breeding more rapid and will allow monitoring of PCN for resistance-breaking populations that contain changed versions of the avirulence genes.

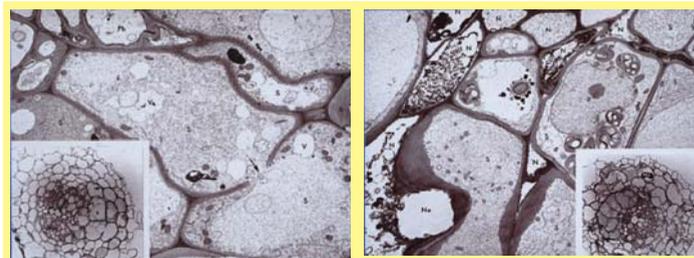


Figure 3: Development of nematode feeding sites in susceptible (left panel) and resistant (right panel) plants. Resistant plants carry the *Hero* gene which confers resistance against a range of cyst nematodes. Susceptible plants support development of large, cytoplasmically enriched feeding sites. In resistant plants a layer of dead cells surrounds the syncytium, restricting the flow of nutrients to the nematode

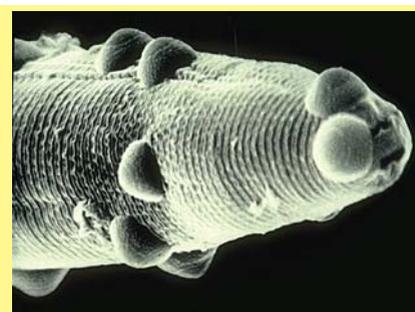
### Biological control

Natural enemies and pathogens of nematodes offer the potential for biological control in some situations.

The genome of one important biological control agent (*Pasteuria penetrans* - Figure 4) is also being sequenced in a collaboration between Rothamsted and NC State University in the USA.

The availability of this sequence and that of *G. pallida* will allow dissection of the interaction between these organisms. Of particular interest are the mechanisms underlying recognition and binding of *Pasteuria* to PCN. This information will improve the prospects for biological control of *G. pallida*.

Figure 4: Binding of spores of the biological control agent *Pasteuria penetrans* to the anterior tip of a juvenile plant parasitic nematode.



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